

Amendments to the Claims

Claims 1-171 (cancelled)

Claim 172 (currently amended) A method of [improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises a chimeric gene selected from the group consisting of] feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a second polypeptide selected from [SEQ ID NOS:9 or 11] SEQ ID NO:9, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase] subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or [subfragment] subsequence, operably linked to [suitable] at least one regulatory [sequences] sequence;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a second polypeptide selected from [SEQ ID NOS:9 or 11] SEQ ID NO:9, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase] subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or [subfragment] subsequence, and (b) an isolated nucleic acid fragment comprising a corn oleosin promoter [wherein said promoter can be full length or partial and said promoter : (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (ii)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions] consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49 [, operably linked to suitable regulatory sequences];

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least [80%] 90% based on the Clustal method of

alignment when compared to a second polypeptide selected from [SEQ ID NOS:9 or 11] SEQ ID NO:9, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase] subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or [subfragment] subsequence, and (b) a shrunken 1 intron/exon, operably linked to [suitable] at least one regulatory sequence [sequences]; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a second polypeptide selected from [SEQ ID NOS:9 or 11] SEQ ID NO:9, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase] subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or [subfragment] subsequence, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter [wherein said promoter can be full length or partial and said promoter : (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (ii)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences,] consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49 ; and (c) a shrunken 1 intron/exon[, operably linked to suitable regulatory sequences]; wherein expression of the chimeric gene results in an altered corn stearic acid phenotype.

Claims 173 (currently amended) A method [of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises a chimeric gene selected from the group consisting of] feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in [SEQ ID NOS: 1 or 2] SEQ ID NO:1, or a [functionally equivalent subfragment of the isolated nucleic acid fragment

encoding a corn delta-12 desaturase] subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of either the fragment or [subfragment] subsequence, operably linked to [suitable] at least one regulatory [sequences] sequence;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in [SEQ ID NOS: 1 or 2] SEQ ID NO:1, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase], subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of either the fragment or [subfragment] subsequence and (b) an isolated nucleic acid fragment comprising a corn oleosin promoter [wherein said promoter can be full length or partial and said promoter : (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (ii)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions] consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49], operably linked to suitable regulatory sequences];

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in [SEQ ID NOS: 1 or 2] SEQ ID NO:1, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase], subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of either the fragment or [subfragment] subsequence, and (b) a shrunken 1 intron/exon, operably linked to [suitable] at least one regulatory [sequences] sequence; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in [SEQ ID NOS: 1 or 2] SEQ ID NO:1, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase], subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous

gene encoding a corn delta-12 desaturase, or the complement of either the fragment or [subfragment] subsequence, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter [wherein said promoter can be full length or partial and said promoter : (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (ii)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions] consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (c) a shrunken 1 intron/exon[, operably linked to suitable regulatory sequences]; wherein expression of the chimeric gene results in an altered corn oleic acid phenotype.

Claim 174 (currently amended) A method of [improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises a chimeric gene selected from the group consisting of] feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of:

(i) a first chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a second polypeptide selected from [SEQ ID NOS:9 or 11] SEQ ID NO:9, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase] subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or [subfragment] subsequence, and linked to a second chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in [SEQ ID NOS: 1 or 2] SEQ ID NO:1, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 stearoyl ACP desaturase, or the complement of either the fragment or subfragment] subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of either the fragment or [subfragment] subsequence, operably linked to [suitable] at least one regulatory [sequences] sequence;

(ii) a chimeric gene comprising (a) [an] a first isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a second polypeptide selected from [SEQ ID NOS:9 or 11] SEQ ID NO:9, or a subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or [subfragment] subsequence, (b) a [chimeric gene comprising an] second isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in [SEQ ID NOS: 1 or 2] SEQ ID NO:1, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment] subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of either the fragment or [subfragment] subsequence, and (c) [an] a third isolated nucleic acid fragment comprising a corn oleosin promoter [wherein said promoter can be full length or partial and said promoter : (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (ii)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions] consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49], operably linked to suitable regulatory sequences];

(iii) a chimeric gene comprising (a) [an] a first isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a second polypeptide selected from [SEQ ID NOS:9 or 11] SEQ ID NO:9, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or subfragment] subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or [subfragment] subsequence, (b) a [chimeric gene comprising an] second isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in [SEQ ID NOS: 1 or 2] SEQ ID NO:1, or a [functionally equivalent

subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment] subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of either the fragment or [subfragment] subsequence, and (c) a shrunken 1 intron/exon, operably linked to [suitable] at least one regulatory sequence [sequences]; or

(iv) a chimeric gene comprising (a) [an] a first isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a second polypeptide selected from [SEQ ID NOS:9 or 11] SEQ ID NO:9, or the complement thereof, (b) a [chimeric gene comprising an] second isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in [SEQ ID NOS: 1 or 2] SEQ ID NO:1, or the complement thereof, (c) [an] a third isolated nucleic acid fragment comprising a corn oleosin promoter [wherein said promoter can be full length or partial and said promoter : (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (ii)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions] consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and [(c)](d) a shrunken 1 intron/exon[, operably linked to suitable regulatory sequences,] ;

wherein expression of the chimeric gene results in an altered corn oil phenotype.

Claim 175 (currently amended) A method of [improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of a corn grain obtained from a corn plant or plant part which comprises a chimeric gene comprising] feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of :

(a) [an] a first isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in [SEQ ID NOS: 1, 58 or 59] SEQ ID NO:1, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-

12 desaturase, or the complement of either the fragment or subfragment] subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of either the fragment or [subfragment] subsequence, (b) [an] a second isolated nucleic acid fragment comprising a corn oleosin promoter [wherein said promoter can be full length or partial and said promoter : (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (ii)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions] consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (c) a shrunken 1 intron/exon[, operably linked to suitable regulatory sequences];

wherein expression of the chimeric gene results in an altered corn oleic acid phenotype, and

further wherein the corn grain has an oil content in the range from about 6% to about 10% on a dry matter basis and further wherein said oil is comprised of not less than 60% oleic acid of the total oil content of the seed.

Claim 176 (currently amended) A method [of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises] feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of :

(i) a first chimeric gene selected from the group consisting of:

(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a second polypeptide selected from [SEQ ID NOS:9 or 11] SEQ ID NO:9, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase, or the complement of either the fragment or subfragment] subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of either the fragment or [subfragment] subsequence, operably linked to [suitable] at least one regulatory sequence [sequences];

(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase

has an amino acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a second polypeptide selected from [SEQ ID NOS:9 or 11] SEQ ID NO:9, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or subfragment] subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or [subfragment] subsequence, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter [wherein said promoter can be full length or partial and said promoter : (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (ii)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions] consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49], operably linked to suitable regulatory sequences];

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a second polypeptide selected from [SEQ ID NOS:9 or 11] SEQ ID NO:9, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or subfragment,] subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or [subfragment] subsequence, and (b) a shrunken 1 intron/exon, operably linked to [suitable] at least one regulatory sequence [sequences]; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a second polypeptide selected from [SEQ ID NOS:9 or 11] SEQ ID NO:9, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or subfragment] subsequence of SEQ ID NO:9 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or [subfragment] subsequence, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter [wherein said promoter can

be full length or partial and said promoter : (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (ii)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions] consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (c) a shrunken 1 intron/exon[, operably linked to suitable regulatory sequences], and

(ii) a second chimeric gene selected from the set consisting of:

(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in [SEQ ID NOS: 1 or 2] SEQ ID NO:1, or a[functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment,] subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of either the fragment or [subfragment] subsequence, operably linked to [suitable] at least one regulatory [sequences] sequence;

(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in [SEQ ID NOS: 1 or 2] SEQ ID NO:1, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment] subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of either the fragment or [subfragment] subsequence, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter [wherein said promoter can be full length or partial and said promoter : (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (ii)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions] consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49[, operably linked to suitable regulatory sequences];

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in [SEQ ID NOS: 1 or 2] SEQ ID NO:1, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment] subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of either the fragment or [subfragment] subsequence, and (2) a shrunken 1 intron/exon, operably linked to [suitable] at least one regulatory sequence [sequences]; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least [80%] 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in [SEQ ID NOS: 1 or 2] SEQ ID NO:1, or a [functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 stearoyl ACP desaturase, or the complement of either the fragment or subfragment] subsequence of SEQ ID NO:1 having at least 500 nucleotides wherein said subsequence is used to cosuppress an endogenous gene encoding a corn delta-12 desaturase, or the complement of either the fragment or [subfragment] subsequence, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter [wherein said promoter can be full length or partial and said promoter : (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (ii)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions] consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (c) a shrunken 1 intron/exon[, operably linked to suitable regulatory sequences], wherein expression of the chimeric genes results in an altered corn oil phenotype.